



Attorney's Docket No. 35800/238853(5800-13B)

PATENT

#4
#4/A

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Inventor: Glucksmann et al. Group Art Unit: Not assigned
Appl. No.: To be Assigned Examiner: Not assigned
Filed: Filed Concurrently Herewith
For: 15625 RECEPTOR, A NOVEL G-PROTEIN COUPLED RECEPTOR

September 26, 2001

REQUEST FOR TRANSFER OF COMPUTER READABLE FORM OF SEQUENCE
LISTING UNDER 37 CFR §1.821(e) AND MPEP 2422.05

RECEIVED

Box Patent Application
Commissioner for Patents
Washington, DC 20231

FEB 25 2005

TECH CENTER 1600/2900

Sir:

Applicants hereby request transfer of previously filed sequence information into the above-mentioned application, concurrently filed herewith.

I hereby state that the paper copy of the sequence listing included in the specification of the above-mentioned application is identical to the computer-readable copy of the sequence listing filed in U.S. Application No. 09/187,134, filed on November 6, 1998. In accordance with 37 CFR §1.821(e) and MPEP 2422.05, please use the only filed computer-readable form filed in that application as the computer-readable form for the above-mentioned application. It is understood that the Patent and Trademark Office will make the necessary change in application number and filing date for the present application.

Respectfully submitted,

Kathryn L. Coulter

Kathryn L. Coulter
Agent for Applicant
Registration No. 45,889

Customer No. 00826
Alston & Bird LLP
Bank of America Plaza
101 South Tryon Street, Suite 4000
Charlotte, NC 28280-4000
Tel Raleigh Office (919) 862-2200
Fax Raleigh Office (919) 862-2260

"Express Mail" Mailing Label Number EL868637424US
Date of Deposit: September 26, 2001
I hereby certify that this paper or fee is being deposited with the United States Postal Service "Express Mail Post Office to Addressee" service under 37 CFR 1.10 on the date indicated above and is addressed to Box Patent Application, Commissioner for Patents, Washington, DC 20231.

Nora C. Martinez
Nora C. Martinez

SEQUENCE LISTING



<110> Glucksmann, Maria A.
Gu, Wei

<120> 15625 Receptor, A Novel G-Protein Coupled Receptor

<130> 5800-13, 035800-171548

<140> 09/187,134

<141> 1998-11-06

<160> 5

<170> PatentIn Ver. 2.0

<210> 1

<211> 342

<212> PRT

<213> Homo sapiens

<400> 1

Met Gln Ala Val Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu
1 5 10 15

Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
20 25 30

Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Gly Leu Ala Met Arg
35 40 45

Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
50 55 60

Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
65 70 75 80

Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
85 90 95

Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
100 105 110

Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
115 120 125

Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
130 135 140

RECEIVED

FEB 25 2005

TECH CENTER 1600/2900

Ser Val Val Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
145 150 155 160

Ile Leu Thr Asn Arg Gln Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
165 170 175

Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
180 185 190

Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
195 200 205

Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
210 215 220

Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
225 230 235 240

Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
245 250 255

Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Thr Ala
260 265 270

Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser
275 280 285

Leu Asn Ala Cys Leu Asp Pro Phe Ile Tyr Phe Phe Leu Cys Lys Ser
290 295 300

Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr
305 310 315 320

Ser Leu Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro
325 330 335

Asn Glu Glu Thr Pro Met
340

<210> 2

<211> 2286

<212> DNA

<213> Homo sapiens

<400> 2

cgctccgtagc tttagagcca gtgtttgaag acaatctctg attgtgaagc cctctttttc 60

tctccttcta tttctctcta gagcaactcaa gactttactg acgaaaactc aggaaatcct 120
 ctatcacaaa gaggtttggc aactaaacta agacattaaa aggaaaatac cagatgccac 180
 tctgcaggct gcaataacta ctacttactg gatacattca aaccctccag aatcaacagt 240
 tatcaggtaa ccaacaagaa atgcaagccg tcgacaacct cacctctgcg cctgggacca 300
 ccagtctgtg caccagagac tacaaaatca cccaggtcct cttccactg ctctacactg 360
 tcctgttttt tgttgactt atcacaaatg gcctggcgat gaggattttc tttcaaatcc 420
 ggagtaaate aaactttatt atttttctta agaacacagt ctttctgat cttctcatga 480
 ttctgacttt tccattcaaa attcttagtg atgccaaact gggaacagga ccaactgagaa 540
 cttttgtgtg tcaagttacc tccgtcatat tttatttcac aatgtatata agtatttcac 600
 tcctgggact gataactatc gatcgctacc agaagaccac caggccattt aaaacatcca 660
 accccaaaaa tctcttgggg gctaagattc tctctgttgt catctgggca ttcattgttct 720
 tactctcttt gcctaacatg attctgacca acaggcagcc gagagacaag aatgtgaaga 780
 aatgctcttt ccttaaatca gagttcgggc tagtctggca tgaaatagta aattacatct 840
 gtcaagtcac tttctggatt aattttctta ttgttattgt atgttatata ctcattacaa 900
 aagaactgta cgggtcatat gtaagaacga ggggtgtagg taaagtcccc aggaaaaagg 960
 tgaacgtcaa agttttcatt atcattgctg tattctttat ttgttttgtt cttttccatt 1020
 ttgcccgaat tccttacacc ctgagccaaa cccgggatgt ctttgactgc actgctgaaa 1080
 atactctgtt ctatgtgaaa gagagcactc tgtgggtaac ttccttaaat gcatgcctgg 1140
 atccgttcac ctattttttc ctttgcaagt ccttcagaaa ttccttgata agtatgctga 1200
 agtgccccaa ttctgcaaca tctctgtccc aggacaatag gaaaaaagaa caggatggtg 1260
 gtgacccaaa tgaagagact ccaatgtaaa caaattaact aaggaaatat ttcaatctct 1320
 ttgtgttcag aactcgtaa agcaaagcgc taagtataaa tattaactga cgaagaagca 1380
 actaagttaa taataatgac tctaaagaaa cagaagatta caaaagcaat tttcatttac 1440
 ctttccagta tgaaaagcta tcttaaaata tagaaaacta atctaaactg tagctgtatt 1500
 agcagcaaaa caaacgacat ccaattgtca tgctgcatgc aaaactacac agaattcatg 1560
 ttttgagag ttttgccaaa atgagtaatc atataatatt tactgtaatt tttaaaatac 1620
 attatcgttc acaattttat tttttcataa tcaactaagg aagaacgatc aattggatat 1680
 aattttctac caaaaatgat agttaaaatg tatatatatc ctagtcccct aaccaaattc 1740
 tgacctattg ggatacttat aaaaatttaa gtaagtggga tacacaaaga ataataacta 1800
 ttaacttttc attattagca aaacctaag ggatttaaac taattgaaac tgtatttgat 1860
 tggacttaat tttttatgtt tatttagaag ataaagattt aaagaagacc tttacaataa 1920
 agagaagaaa tatcgaagtc attaaaataa ggagacttac ttttatgaca ttctaatact 1980
 aaaaaatata gaaatatatt ctttaattcta gagaaactag ttttactaat tttttacaac 2040
 ttcaataata ccatcactga cacttacctt tattaattag cttctagaaa atagctgcta 2100
 attaggttaa tgaacatttt accttagtga aaaaaattaa ttaaatatga ttacaaagtt 2160
 gcacagcata actactgaga ggaaagtgat tgatctgttt gtaattactt gtttgtattg 2220
 gtgtgtataa aatacaaaat ttacattaaa ctctaaaaaa aaaaaaaaaa aaaaaaaaaa 2280
 gggcgg 2286

<210> 3

<211> 342

<212> PRT

<213> Macaca sp.

<400> 3

Met Gln Ala Ile Asp Asn Leu Thr Ser Ala Pro Gly Asn Thr Ser Leu

1

5

10

15

Cys Thr Arg Asp Tyr Lys Ile Thr Gln Val Leu Phe Pro Leu Leu Tyr
 20 25 30

Thr Val Leu Phe Phe Val Gly Leu Ile Thr Asn Ser Leu Ala Met Arg
 35 40 45

Ile Phe Phe Gln Ile Arg Ser Lys Ser Asn Phe Ile Ile Phe Leu Lys
 50 55 60

Asn Thr Val Ile Ser Asp Leu Leu Met Ile Leu Thr Phe Pro Phe Lys
 65 70 75 80

Ile Leu Ser Asp Ala Lys Leu Gly Thr Gly Pro Leu Arg Thr Phe Val
 85 90 95

Cys Gln Val Thr Ser Val Ile Phe Tyr Phe Thr Met Tyr Ile Ser Ile
 100 105 110

Ser Phe Leu Gly Leu Ile Thr Ile Asp Arg Tyr Gln Lys Thr Thr Arg
 115 120 125

Pro Phe Lys Thr Ser Asn Pro Lys Asn Leu Leu Gly Ala Lys Ile Leu
 130 135 140

Ser Val Leu Ile Trp Ala Phe Met Phe Leu Leu Ser Leu Pro Asn Met
 145 150 155 160

Ile Leu Thr Asn Arg Arg Pro Arg Asp Lys Asn Val Lys Lys Cys Ser
 165 170 175

Phe Leu Lys Ser Glu Phe Gly Leu Val Trp His Glu Ile Val Asn Tyr
 180 185 190

Ile Cys Gln Val Ile Phe Trp Ile Asn Phe Leu Ile Val Ile Val Cys
 195 200 205

Tyr Thr Leu Ile Thr Lys Glu Leu Tyr Arg Ser Tyr Val Arg Thr Arg
 210 215 220

Gly Val Gly Lys Val Pro Arg Lys Lys Val Asn Val Lys Val Phe Ile
 225 230 235 240

Ile Ile Ala Val Phe Phe Ile Cys Phe Val Pro Phe His Phe Ala Arg
 245 250 255

Ile Pro Tyr Thr Leu Ser Gln Thr Arg Asp Val Phe Asp Cys Ala Ala
 260 265 270

Glu Asn Thr Leu Phe Tyr Val Lys Glu Ser Thr Leu Trp Leu Thr Ser
 275 280 285

Leu Asn Ala Cys Leu Asp Pro Phe Thr Tyr Phe Phe Leu Cys Lys Ser
 290 295 300

Phe Arg Asn Ser Leu Ile Ser Met Leu Lys Cys Pro Asn Ser Ala Thr
 305 310 315 320

Ser Gln Ser Gln Asp Asn Arg Lys Lys Glu Gln Asp Gly Gly Asp Pro
 325 330 335

Asn Glu Glu Thr Pro Met
 340

<210> 4

<211> 2272

<212> DNA

<213> Macaca sp.

<400> 4

acgcgtccgc aatctctgat tgtaaagccc tctcttctctc tccttctatt tctctataga 60
 aactcaaga ctttactgat gaaaactcag gaaattctct atcacaaga ggtttgcaa 120
 cttaaactaag acattaaaag gaaaatacca gatgccactc tgcacgttgc aataactact 180
 atttactgga tacattcaaa tctccagaa tcaacggtta tcaggtaacc aacaagaaat 240
 gcaagccatc gacaacctca cgtctgcgcc tgggaacacc agtctgtgca ccagagacta 300
 caaaatcacc caggctctct tccactgct ctacactgtc ctgttttttg ttggactcat 360
 cacaatatgc ctggcgatga ggattttctt tcaaattcgg agtaaataca actttattat 420
 ttttcttaag aacacagtca ttccgatct tctcatgatt ctgacttttc cattcaaaat 480
 tcttagtgat gccaaactgg gaacaggacc actgagaact tttgtgtgtc aagttacctc 540
 cgtcatatct tatttcacaa tgtatatcag tatttcattc ctgggactga taactatcga 600
 tcgctaccag aagaccacca ggccatttaa aacatccaac cccaaaaatc tcttgggggc 660
 taagattctc tctgttctca tctgggcatt catgttctta ctctctttgc ctaacatgat 720
 tctgactaac aggcggccaa gagacaagaa tgtgaagaaa tgcctttcc ttaaatacaga 780
 gttcggccta gtctggcatg aaatagtaaa ttacatctgt caagtcattt tctggattaa 840
 tttcttaatt gtcattgtat gttacacact cattacaaa gaactgtacc ggtcatatgt 900
 aagaacaagg ggtgtaggta aagtccccag gaaaaagggtg aacgtcaaa ttttcattat 960
 cattgctgta ttctttattt gttttgttcc ttccatttt gccgaattc cttataacct 1020
 gagccaaaacc cgggatgtct ttgactgcgc cgtgaaaaat actctgttct atgtgaaaga 1080
 gagtactctg tggtaactt cttaaatgc atgcctggat ccgttcacct attttttctt 1140
 ttgcaagtcc ttcagaaatt cttgataag tatgctgaag tgcccaatt ctgcaacatc 1200
 tcagtcccag gacaatagga aaaaagaaca ggatggtggt gacccaaatg aagagactcc 1260
 aatgtaaaca tattaactga ggaaatatgt caatctcttt gcgttcagaa ctcatataag 1320
 caaagcgcta cgtaaaaata ttaactgacg aagaagcaac tgagttaata acaatgactc 1380
 ttaaaacatg taatagaaga ttacaaaag caattttcat ttacctttcc agtatgaaaa 1440
 gctatgtaa aatatagaaa actaatctaa cctgtagctg tatagtatca aaacaaatga 1500
 catccaattg gcatgctgca tgcaaaaacta cacagaattc acgttttgca gagttttgcc 1560

aaaatgagta atcatataat atctaccgta atgttttaaaa tacattattg ctcacgattt 1620
 tattttcttca taatcaacta aggaagaatt atcaattgga tacaatcttc ttacaaaaaa 1680
 tgacacttaa aatgtatata tatcctagcc cctaaccaaa tcctgaccta ttgggatact 1740
 tataaaaaatt tgagtaagtg ggatacacaa agaataataa ctattaactt ttaattatga 1800
 gcaaaaaacct aagggttaaa tttaaactaa ttgaaactgt atttgattgg acttaatttt 1860
 tttgtttatt aagaagacac ttgaagaaga cctttacaat aaagagaaga aatatcaaag 1920
 tcattaaaat aaggagagtt acttttatga tattctaaca ctaaacaata tagaaatatt 1980
 tccttaatat tagtttctag agaaactagt ttactaatt ttttacaacc tcaataatac 2040
 catcattgac acttaccttt attaactagc ttctagaaaa tacctgctaa ttaggttaat 2100
 gaacatttta tgttagtga aaaaattaat taaatatgat taciaaagtg cacagcataa 2160
 ctactgaaag tgattgatcc atttgttaatt atttgtttgt actggtgtgt ataaaaatata 2220
 aaatttacat taaactctaa atcaccaaaa aaaaaaaaaa aaaaaagggc gg 2272

<210> 5

<211> 269

<212> PRT

<213> Unknown

<220>

<223> Description of Unknown Organism: Rhodopsin family
transmembrane receptor

<400> 5

Gly Asn Ile Leu Val Ile Trp Val Ile Cys Arg Tyr Arg Arg Met Arg
 1 5 10 15

Thr Pro Met Asn Tyr Phe Ile Val Asn Leu Ala Val Ala Asp Leu Leu
 20 25 30

Phe Ser Leu Phe Thr Met Pro Phe Trp Met Val Tyr Tyr Val Met Gly
 35 40 45

Gly Arg Trp Pro Phe Gly Asp Phe Met Cys Arg Ile Trp Met Tyr Phe
 50 55 60

Asp Tyr Met Asn Met Tyr Ala Ser Ile Phe Phe Leu Thr Cys Ile Ser
 65 70 75 80

Ile Asp Arg Tyr Leu Trp Ala Ile Cys His Pro Met Arg Tyr Met Arg
 85 90 95

Trp Met Thr Pro Arg His Arg Ala Trp Val Met Ile Ile Ile Ile Trp
 100 105 110

Val Met Ser Phe Leu Ile Ser Met Pro Pro Phe Leu Met Phe Arg Trp
 115 120 125

Ser Thr Tyr Arg Asp Glu Asn Glu Trp Asn Met Thr Trp Cys Met Ile

130

135

140

Tyr Asp Trp Pro Glu Trp Met Trp Arg Trp Tyr Val Ile Leu Met Thr
145 150 155 160

Ile Ile Met Gly Phe Tyr Ile Pro Met Ile Ile Met Leu Phe Cys Tyr
165 170 175

Trp Arg Ile Tyr Arg Ile Ala Arg Leu Trp Met Arg Met Ile Pro Ser
180 185 190

Trp Gln Arg Arg Arg Arg Met Ser Met Arg Arg Glu Arg Arg Ile Val
195 200 205

Lys Met Leu Ile Ile Ile Met Val Val Phe Ile Ile Cys Trp Leu Pro
210 215 220

Tyr Phe Ile Val Met Phe Met Asp Thr Leu Met Met Trp Trp Phe Cys
225 230 235 240

Glu Phe Cys Ile Trp Arg Arg Leu Trp Met Tyr Ile Phe Glu Trp Leu
245 250 255

Ala Tyr Val Asn Cys Pro Cys Ile Asn Pro Ile Ile Tyr
260 265